

| | | |
|-----------|-----------|----------|
| APPROVED | O.G. FIG. | |
| BY | CLASS | SUBCLASS |
| DRAFTSMAN | | |

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ovary
liver
muscle
testis
spleen
intestine
pancreas
seminal vesicle
kidney
brain
thymus
lung
heart

FIG. 1

| | | |
|-----------|-----------|----------|
| APPROVED | O.G. FIG. | |
| BY | CLASS | SUBCLASS |
| DRAFTSMAN | | |

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| | | |
|-----|---|-----|
| 1 | CGGGCCAGGAGGAGGACCCCCACCTGTGACCCCTGCCACCCCTTATGTTGCAGGCCAGAC | 60 |
| | R A R R R T P T C E P A T P L C C R R D | |
| 61 | CATTACGTAGACTTCCAGGAACCTGGATGGCGGGACTGGATACTGCAGCCCCAGGGGTAC | 120 |
| | H Y V D F Q E L G W R D W I L Q P E G Y | |
| 121 | CAGCTGAATTACTGCAGTGGCAGTGCCCTCCCCACCTGGCTGGCAGCCCAGGCATTGCT | 180 |
| | Q L N Y C S G Q C P P H L A G S P G I A | |
| 181 | GCCTCTTCCATTCTGCCGTCTCAGCCTCCCTCAAAGCCAACAATCCTGGCCTGCCAGT | 240 |
| | A S F H S A V F S L L K A N N P W P A S | |
| 241 | ACCTCCTGTTGTGTCCTACTGCCGAAGGCCCTCTCTCTACCTGGATCATAAT | 300 |
| | T S C C V P T A R R P L S L L Y L D H N | |
| 301 | GGCAATGTGGTCAAGACGGATGTGCCAGATAATGGTGGTGGAGGCCTGTGGCTGCAGCTAG | 360 |
| | G N V V K T D V P D M V V E A C G C S * | |

FIG. 2

DRAFTED BY DRAFTSMAN

Family member % identity with GDF-12

| | |
|--------------------|----|
| GDF-1 | 43 |
| GDF-3 | 36 |
| GDF-5 | 36 |
| GDF-6 | 39 |
| GDF-7 | 42 |
| GDF-9 | 30 |
| BMP-3 | 37 |
| BMP-2 | 43 |
| BMP-4 | 42 |
| Vgr-1 | 41 |
| OP-1 | 40 |
| BMP-5 | 38 |
| OP-2 | 39 |
| MIS | 30 |
| Inhibin- α | 27 |
| Inhibin- β A | 47 |
| Inhibin- β B | 50 |
| Nodal | 38 |
| GDNF | 21 |
| TGF- β 1 | 36 |
| TGF- β 2 | 36 |
| TGF- β 3 | 41 |

FIG. 4

| | | |
|-----------|-----------|----------|
| APPROVED | O.G. FIG. | |
| BY | CLASS | SUBCLASS |
| CRAFTSMAN | | |

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1 GAGCTGTGACGGTCAAGCACAGCTATCCATCAGATGATCTACTTTCAGGCCCTTGAGTC 60
 61 CCAGACAATAGAACAGACAGGTGGCTGTACCCCTGGCCAAGGGTAGGTGTCGGCAGTGGTGTGTC 120
 121 TGCTGTCACTGTGCCCTCATGGCCCCAGCAATCAGACTCAACAGACGGAGCAACTGCC 180
 181 ATCCGAGGCTCTGAACCAGGGCATTCAACCAGGAGCATGGGCTCCGTATGTCAGCT 240
 M R L P D V Q L
 241 CTGGCTGGTGCTGTGGCACTGGTGGAGCACAGGGACAGGGCTGTGTGTCCTC 300
 W L V L L W A L V R A Q G T G S V C P S
 301 CTGTGGGGCTCCAAACTGGCACCCAAAGCAGAACGAGCTCTGGTGTGGAGCTAGCCAA 360
 C G G S K L A P Q A E R A L V L E L A K
 361 GCAGCAAATCCTGGATGGGTTGCACCTGACCGACTCGTCCCAGAATAACTCATCCTCCACC 420
 Q Q I L D G L H L T S R P R I T H P P P
 421 CCAGGCAGGGCTGACCAGAGCCCTCCGGAGACTACAGCCAGGGAGTGTGGCTCCAGGGAA 480
 Q A A L T R A L R R L Q P G S V A P G N
 481 TGGGGAGGAGGTCACTCAGCTTGCTACTGTCACAGACTCCACTTCAGCCTACAGCTCCCT 540
 G E E V I S F A T V T D S T S A Y S S L
 541 GCTCACTTTCACCTGTCCACTCCTCGGCCCCACCACCTGTACCATGCCCGCTGTGGCT 600
 L T F H L S T P R S H H L Y H A R L W L
 601 GCACGTGCTCCCCACCCCTTCCGGCACTCTTGCTTGAGGATCTTCCGATGGGACCAAG 660
 H V L P T L P G T L C L R I F R W G P R
 661 GAGGAGGGCCAAGGGTCCCGACTCTCTGGCTGAGCACCACATACCAACCTGGGCTG 720
 R R R Q G S R T L L A E H H I T N L G W
 721 GCATACCTTAACCTGCCCCCTAGTGGCTTGAGGGTGAGAAGTCTGGTGTCTGAAACT 780
 H T L T L P S S G L R G E K S G V L K L
 781 GCAACTAGACTGCAGACCCCTAGAAGGCAACAGCACAGTTACTGGACAACCGAGGGCT 840
 Q L D C R P L E G N S T V T G Q P R R L
 841 CTTGGACACAGCAGGACACCAGCAGCCCTCTAGAGCTTAAGATCCGAGCCAATGAGCC 900
 L D T A G H Q Q P F L E L K I R A N E P
 901 TGGACCAGGGGGCCAGGAGGAGGACCCCCCACCTGTGAGCCTGCGACCCCTTATGTTG 960
 G A G R A R R R R T P T C E P A T P L C C
 961 CAGGGAGGACCATACGTAGACTTCCAGGAACCTGGGATGGGGGACTGGATACTGCAGCC 1020
 R R D H Y V D F Q E L G W R D W I L Q P
 1021 CGAGGGGTACCAAGCTGAATTACTGCAGTGGGAGTGGCCCTCCCCACCTGGCTGGCAGCCC 1080
 E G Y Q L N Y C S G Q C P P H L A G S P
 1081 AGGCATTGCTGCCCTTTCCATTCTGCCGCTTCAGCCTCCTCAAAGCCAACAATCCTTG 1140
 G I A A S F H S A V F S L L K A N N P W
 1141 GCCTGCCAGTACCTCCGTGTTGTGCTCCACTGCCCGAAGGCCCTCTCTCCTCTACCT 1200
 P A S T S C C V P T A R R P L S L L Y L
 1201 GGATCATATAATGGCAATGTGGTCAAGACGGATGTGCCAGATATGGTGGTGGAGGCCGTG 1260
 D H N G N V V K T D V P D M V V E A C G
 1261 CTGGCAGCTAGCAAGAGGACCTGGGCTTGGAGTGAAGAGACCAAGATGAAGTTCCCAG 1320
 C S *
 1321 GCACAGGGCATCTGTGACTGGAGGCATCAGATTCTGTACCCACACCCAAACCAACACC 1380
 1381 ACCTGGCAATATGACTCACTTGACCCCTATGGGACCCAAATGGGACTTTCTGTGAG 1440
 1441 ACTCTGGCTTATTCCAGGTTGGCTGATGCTTGAGATGGTAAAGCGTTCTCTAA 1500
 1501 GGGGTCTACCCAGAAAGCATGATTCTGCCCTAAGTCTGTGAGAACAGATGTCACGGACT 1560
 1561 AGGGAGGGAGGGACGGAAAGCAGAGAAAAATTACTTAGCCTCTCCAAAGATGAGAAAGTC 1620
 1621 CTCAAGTGAGGGAGGAGGAAGCAGATAGATGGTCCAGCAGGCTTGAGCAGGGTAAGCA 1680
 1681 GGCTGGCCCAAGGGTAAAGGCTGTTGAGGTACCTTAAGGGAAAGGTCAAGAGGGAGATGGC 1740
 1741 AAGGCCTGAGGGAGGATGCTTACGGGACCCCCAGAAACAGGAGTCAGGAAAATGAGGCA 1800
 1801 CTAAGCCTAAGAAGTTCCCTGGTTTCTCAGGGACAGGACCCACTGGGAGACAAGCAT 1860
 1861 TTATACCTTTCTCTTTTATTTTGTGAGATCGAGTCTGCTCTGTCACCAGGCT 1920
 1921 GGAGTGCAGTGACACGATCTGGCTCACTGCAACCTCCGTCTCTGGGTTCAAGTGATT 1980
 1981 TTCTGCCCTCAGCCTCCGAGCAGCTGGGATTACAGCGCCCACTAATTGTTGATTCTTA 2040
 2041 GTAGAAACGGAGGTTCAACATGTTGGCAGGATGGCTCAATCTCTTGACCTCTGATCC 2100
 2101 ACCCGACTTGGCCTCCCGAAGTGATGAGATTATAGCGTGAGCCACCGCGCCTGGCTTAT 2160
 2161 ACTTTCTTAATAAAAAGGAGAAGAAAATCAACAAATGTGAGTCATAAAGAAGGGTTAGG 2220
 2221 GTGATGGTCCAGAGCAACAGTCTTCAGTGTACTCTGTAGGCTTCTGGGAGGTCCCTT 2280
 2281 TCAGGGGTGTCCACAAAGTCAAAGCTATTCTCATATAACTAACATGTTATTGCTT 2340
 2341 TTGAATTCTCATTATCTTAAATTGTATTGAGTTCCAGAGGCCGTGACATGTG 2400
 2401 ATTACATCATCTTGAC 2419